

ABSTRACT

The present invention provides a variety of related proteomics analytical modalities that are open-ended, rapid, convenient and suitable for implementation in a high throughput parallel assay system. Specificity-determining compositions and methods are disclosed for use in proteomics. These compositions and methods provide a protein resolved from other protein species contained in a sample fluid, in its native, biologically functional conformation. The present invention provides a specificity-determining substrate that forms a complex with a protein molecule in a homogenous fashion. The specificity-determining substrate includes a specificity-determining ligand bound to a support, wherein optionally the substrate further includes a spacer bound between the ligand and the support. In addition a complex is provided that includes a specificity-determining substrate and a protein molecule. Furthermore, an array including a plurality of loci is provided, in which each locus includes a specificity-determining substrate of the invention. These substrates, complexes and arrays may be employed in a method of resolving a first protein from a fluid including one or more species of native, biologically active protein molecules, wherein the first protein retains its native structure and its biological activity; in a method of purifying one or more first proteins from a fluid including one or more species of native, biologically active protein molecules, wherein the purified first protein retains its native structure and its biological activity; in a method of characterizing one or more proteins in a fluid including one or more species of protein molecule; and in a method of identifying one or more proteins in a sample fluid wherein the concentration of the one or more proteins in the sample fluid differs from the concentration of the one or more proteins in a reference fluid.